SEQUENCE LISTING

<110> Moore et al.

<120> Human Transcription Factor IIA

<130> PF135D2

<150> PCT/US94/10644
<151> 1994-09-20

<150> US 08/411,635
<151> 1995-04-11

<150> US 08/845,011
<151> 1997-04-22

<160> 5

<170> PatentIn version 3.1

<210> 1
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (190)..(519)
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gtggtcggag aagtaggaac ctcctgccgg gctcgtggcg gcttctgtcc gctccgcgga 120

gggaagcgcc ttccccacag gacatcaatg caagcttgaa taagaaaaac aaattcttcc 180

tcctaagcc atg gca tat cag tta tac aga aat act act ttg gga aac agt 231
Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser
1 5 10

ctt cag gag agc cta gat gag ctc ata cag tct caa cag atc acc ccc 279
Leu Gln Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro
15 20 25 30

caa ctt gcc ctt caa gtt cta ctt cag ttt gat aag gct ata aat gca 327
Gln Leu Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala
35 40 45

gca ctg gct cag agg gtc agg aac aga gtc aat ttc agg ggc tct cta 375
Ala Leu Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu
50 55 60

aat acg tac aga ttc tgc gat aat gtg tgg act ttt gta ctg aat gat 423
Asn Thr Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp
65 70 75

gtt gaa ttc aga gag gtg aca gaa ctt att aaa gtg gat aaa gtg aaa 471
Val Glu Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys
80 85 90

att gta gcc tgt gat ggt aaa aat act ggc tcc aat act aca gaa tga 519
Ile Val Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu
95 100 105

atagaaaaaa tatgactttt ttacaccatc ttctgttatt cattgctttt gaagagaagc 579

atagaagaga ctttttattt attctagaat tgcagaaatg actacactgt gctaraccag 639

agaattccag tagaaagaaa cttgtaactc tgtagcctct tacatcacct ttattataca 699

gcatgaaaaa ccataacttt tttttaagga caaaagttgt tgccttccta agaaccttct 759

ttaataaact cattttaaaa ctctgaaaaa aaaaaaaaaa aaaaa 804

<210> 2
<211> 109
<212> PRT
<213> Homo sapiens

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Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser Leu Gln
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Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro Gln Leu
20 25 30

Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala Ala Leu
35 40 45

Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu Asn Thr
50 55 60

Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp Val Glu
65 70 75 80

Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys Ile Val
85 90 95

Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu
100 105

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<211> 29
<212> DNA
<213> Artificial sequence

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<223> Contains a Bam HI restriction enzyme site

<400> 3
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<210> 4
<211> 26
<212> DNA
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<223> Contains complementary sequences to a HindIII site

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gcggcaagct tattctgtag tattgg 26

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<212> PRT
<213> Saccharomyces cerevisiae

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Met Ala Val Pro Gly Tyr Tyr Glu Leu Tyr Arg Arg Ser Thr Ile Gly
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Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile
20 25 30

Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val
35 40 45

Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly
50 55 60

Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val
65 70 75 80

Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln
85 90 95

Asn Gly Ser Gly Asp Ser Ser Val Ile Ser Val Asp Lys Leu Arg Ile
100 105 110

Val Ala Cys Asn Ser Lys Lys Ser Glu
115 120